

GAATTCCAGTGTGCTGGCTTCTCCTCACCTGCAGACACACACTCCTTTGGGCAAGACCTGAGACCCCTTGCTAAGTC

1
AAGAGCCTCAATGGGCTGCAGAGAAGACTAGAGAAGACCAAGCAAGCC MET ILE PHE PRO TRP LYS
ATG ATA TTT CCA TGG AAA TGT

10
GLN SER THR GLN ARG ASP LEU TRP ASN ILE PHE LYS
CAG AGC ACC CAG AGG GAC TTA TGG AAC ATC TTC AAG
[TGT] TGG TGG GGG TGG ACA ATG CTC [TGT]

30
[CYS] ASP PHE LEU ALA [HIS HIS GLY THR TYR [CYS] TRP THR TYR HIS TYR SER GLU LYS PRO
[TGT] GAT TTC CTG GCA [CAT CAT GCA ACC TAC [TGC] TGG ACT TAC CAT TAT TCT GAA AAA CCC

50
MET ASN TRP GLN ARG ALA ARG ARG PHE [CYS] ARG ASP [ASN TYR THR] ASP LEU VAL ALA ILE
ATG AAC TGG CAA AGG GCT AGA AGA TTC [TGC] CGA GAC [AAT TAC ACA] GAT TTA GTT GCC ATA

70
GLN ASN LYS ALA GLU ILE GLU TYR LEU GLU LYS THR LEU PRO PHE SER ARG SER TYR TYR
CAA AAC AAG GCG GAA ATT GAG TAT CTG GAG AAG ACT CTG CCC TTC AGT CGT TCT TAC TAA

90
TRP ILE GLY ILE ARG LYS ILE GLY GLY ILE TRP THR TRP VAL GLY THR [ASN LYS SER] LEU
TGG ATA GGA ATC CCG AAG ATA GGA GGA ATA TGG ACC TGG GTG GGA ACC [AAC AAA TCT] CTC

110
THR GLU GLU ALA GLU ASN TRP GLY ASP GLY GLU PRO ASN ASN LYS LYS ASN LYS GLU ASP
ACT GAA GAA GCA GAG AAC TGG GGA GAT GGT GAG CCC AAC AAC AAG AAC AAC GAG GAC

130
[CYS] VAL GLU ILE TYR ILE LYS ARG ASN LYS ASP ALA GLY LYS TRP ASN ASP ASP ALA [CYS]
[TGC] GTG GAG ATC TAT ATC AAG AGA AAC AAA GAT GCA GGC AAA TGG AAC GAT GAC GCC [TGT]

150
HIS LYS LEU LYS LYS ALA ALA LEU [CYS] TYR THR ALA SER [CYS] GLN PRO TRP SER [CYS] SER GLY
CAC AAA CTA AAG GCA GGC CTC [TGT] TAC AGA GCT TCT [TGC] CAG CCC TGG TCA [TGC] AGT GCC

FIG. 1A

170 HIS GLY GLU CYS VAL GLU ILE ILE ASN ASN HIS THR CYS ASN CYS ASP VAL GLY TYR TYR
 CAT GGA GAA TGT GTA GAA ATC ATC AAT AAT CAC ACC TGC AAC TGT GAT GTG GGG TAC TAT
 190 GLY PRO GLN CYS GLN LEU VAL ILE GLN CYS GLU PRO LEU GLU ALA PRO GLU LEU GLY THR
 GGG CCC CAG TGT CAG CTT GTG ATT CAG TGT GAG CCT TTG GAG GCC CCA GAG CTG GGT ACC
 210 MET ASP CYS THR HIS PRO PHE GLY ASN PHE SER PHE SER SER GLN CYS ALA PHE SER CYS
 ATG GAC TGT ACT CAC CCC TTT GGA AAC TTC AGC TTC AGC TCA CAG TGT GCC TTC AGC TGC
 230 SER GLU GLY THR ASN LEU THR GLY ILE GLU GLU THR THR CYS GLY PRO PHE GLY ASN TRP
 TCT GAA GGA ACA AAC TTA ACT GGG ATT GAA GAA ACC ACC TGT GGA CCA TTT GGA AAC TGC
 250 SER PRO GLU PRO THR CYS GLN VAL ILE GLN CYS GLU PRO LEU SER ALA PRO ASP LEU
 TCA TCT CCA GAA CCA ACC TGT CAA GTG ATT CAG TGT GAG CCT CTA TCA GCA CCA GAT TTG
 270 GLY ILE MET ASN CYS SER HIS PRO LEU ALA SER PHE SER PHE THR SER ALA CYS THR PHE
 GGG ATC ATG AAC TGT AGC CAT CCC CTG GCC AGC TTC AGC TTT ACC TCT GCA TGT ACC TTC
 290 ILE CYS SER GLU GLY THR GLU LEU ILE GLY LYS LYS LYS THR ILE CYS GLU SER SER GLY
 ATC TGC TCA GAA GGA ACT GAG TTA ATT GGG AAG AAG AAA ACC ATT TGT GAA TCA TCT GGA
 310 ILE TRP SER ASN PRO SER PRO ILE CYS GLN LYS LEU ASP LYS SER PHE SER MET ILE LYS
 ATC TGG TCA AAT CCT AGT CCA ATA TGT CAA AAA TTG GAG AAA AGT TTC TCA ATG ATT AAG
 330 GLU GLY ASP TYR ASN PRO LEU PHE ILE PRO VAL ALA VAL MET VAL THR ALA PHE SER GLY
 GAG GGT GAT TAT AAC CCC CTC TTC ATT CCA GTG GCA GTC ATG GTT ACT GCA TTC TCT GGG

FIG. 1B

STOP TRANSFER SEQUENCE

LEU ALA PHE ILE ILE TRP LEU ALA ARG ARG LEU LYS LYS GLY LYS LYS SER LYS ARG SER
TTG GCA TTP ATC ATT TGG CTG GCA AGG AGA TTA AAA AAA GGC AAG AAA TCC AAG AGA AGT
.....

370 372

MET ASN ASP PRO TYR OC
ATG AAT GAC CCA TAT TAA ATCGCCCTGGTGAAGAAATCTTGAATACTAAAAATCATGAGATCCTTTA

FIG.1C

AATCCTTCCATGAACGTTTGTGTGGTGCCACCTCCTACGTCAAACATGAAGTGTGTTCCCTCAGTGCACTGGCAA
GATTCTACCCGACCAACAGTTCCTTCAGCTTCCATTTCGCCCTCATTTATCCCTCAACCCCAAGCCACAGGTGTT
TATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAAGACCATAAGGAAAGATTTCATGTGAATATAAG
ATGGCTGACTTGTCTTTCTGACTCTGTTTTCAGTTTCAATTCACTGCTGTAATGACAGACACTTCTPAAT
GAAGTCAAAATTGATACATATGTAATATGACTCAGTTTCTTGAGATCAAAATTTCACGTCGTCCTCTGTATACT
GTGAGGTACACTCTTATAGAAAGTCAAAAAGCTACGCTCTCCTTCTTCTAACTCCAGTGAAGTAATGGGGTCC
TGCTCAAGTTGAAGAGTCTATTTGACCTGAGCCGCGCTCTGTGAATTGGACCATCCTATTTAACTGGCTTCAG
GCCTCCCACTCTTCAGCCACCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGAGTGCACAAGCAA
AAGGAGAGAAGAGAAATAGCCCTGCGCGGTTTTAAGTTGGGGGTTTGTCTTCTTTATGAGAACCATTCCT
ATTCTTATAGTCAATGTTCTTTTATCAGCATATTAATTAGTAAACATCAGTGAATGCTAGCTGCAAGTGACA
TCTCTTGTATGTCATATGGAAGATTAAACAGGTGAGAAATTCCTGATTCACAATGAATGCTCTCTTCCCT
GCCCCCAGAACTTTATCCACTTACCTAGATTCTACATATTTTAAATTTCATCTCAGGCTCCCTCAACCCACGG
GGCCGCGCAGCACACTGAATTC

GAATTCTCGAGCTCGTGCAGCAGCCCTCTTGTGCAAGAACTCTGAGCCCCAGGTGCAGAGGCTGAGCCCTGCAGAG

1
10
AGACTGCAGAGAGACCAGCAAGCC MET VAL PHE PRO TRP ARG CYS GLU GLY THR TYR TRP GLY
ATG GTG TTT CCA TGG AGA TGT GAG GGT ACT TAC TGG GGC

FIG.2A

20
30
SER ARG ASN ILE LEU LYS LEU TRP VAL TRP THR LEU LEU CYS CYS ASP PHE LEU ILE HIS
CTG TGG GTC TGG ACA CTG CTC TGT TGT GAC TTC CTG ATA CAC

40
50
N-TERMINUS
HIS GLY THR HIS CYS TRP THR TYR HIS TYR SER GLU LYS PRO MET ASN TRP GLU ASN ALA
CAT GGA ACT CAC TGT TGG ACT TAC CAT TAT TCT GAA AAG CCC ATG AAC TGG GAA AAT GCT

60
70
ARG LYS PHE CYS LYS GLN ASN TYR THR ASP LEU VAL ALA ILE GLN ASN LYS ARG GLU ILE
AGA AAG TTC TGC AAG CAA AAT TAC ACA GAT TTA GTC GCC ATA CAA AAC AAG AGA GAA ATT

80
90
GLU TYR LEU LEU GLU ASN THR LEU PRO LYS SER PRO TYR TYR TRP ILE GLY ILE ARG LYS
GAG TAT TTA GAG AAT ACA TTG CCC AAA AGC CCT TAT TAC TAC TGG ATA GGA ATC AGG AAA

100
110
ILE GLY LYS MET TRP THR TRP VAL GLY THR ASN LYS THR LEU THR LYS GLU ALA GLU ASN
ATT GGG AAA ATG TGG ACA TGG GTG GGA ACC AAC AAA ACT CTC ACT AAA GAA GCA GAG AAC

120
130
TRP GLY ALA GLY GLU PRO ASN ASN LYS LYS SER LYS GLU ASP CYS VAL GLU ILE TYR ILE
TGG GGT GCT GGG GAG CCC AAC AAC AAG AAG TCC AAG GAG GAC TGT GTG GAG ATC TAT ATC

140
150
LYS ARG GLU ARG ASP SER GLY LYS TRP TRP ASN ASP ASP ALA CYS HIS LYS ARG LYS ALA ALA
AAG AGG GAA CGA GAC TCT GGG AAA TGG AAC GAT GAC GCC TGT CAC AAA CGA AAG GCA GCT

LEU [CYS] TYR THR ALA SER 160
 CTC [TGC] TAC ACA GCC TCT [TGC] GLN PRO GLY SER [CYS] ASN GLY ARG GLY GLU [CYS] VAL GLU
 THR ILE ASN [ASN] HIS THR 180
 ACT ATC AAC [AAT] CAC ACG [TGC] ILE [CYS] ASP ALA GLY TYR TYR GLY PRO GLN [CYS] GLN TYR
 VAL VAL GLN [CYS] GLU PRO LEU GLU ALA PRO GLU LEU GLY THR MET ASP 210
 GTG GTC CAG [TGT] GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC [CYS] ILE HIS PRO
 LEU GLY [ASN] PHE SER 220
 TTG GGA [AAC] TTC AGC PHE GLN SER LYS [CYS] ALA PHE [ASN] CYS SER GLU GLY ARG GLU LEU
 LEU GLY THR ALA GLU THR GLN 240
 CTT GGG ACT GCA GAA ACA CAG [TGT] GLY ALA SER GLY [ASN] TRP SER SER PRO GLU PRO ILE
 [CYS] GLN VAL VAL GLN [CYS] GLU PRO LEU GLU ALA PRO GLU LEU GLY THR MET ASP [CYS] ILE
 [TGC] CAA GTG GTC CAG [TGT] GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC [TGC] ATC
 HIS PRO LEU GLY [ASN] PHE SER 280
 CAC CCC TTG GGA [AAC] TTC AGC PHE GLN SER LYS [CYS] ALA PHE [ASN] CYS SER GLU GLY ARG
 GLU LEU LEU GLY THR ALA GLU THR GLN [CYS] GLY ALA SER GLY [ASN] TRP SER SER PRO GLU
 GAG CTA CTT GGG ACT GCA GAA ACA CAG [TGT] GGA GCA TCT GGA [AAC] TGG TCA TCT CCA GAG
 PRO ILE [CYS] GLN GLU THR [ASN] ARG SER PHE SER LYS ILE LYS GLU GLY ASP TYR ASN [PRO]
 CCA ATC [TGC] CAA GAG ACA [AAC] AGA AGT TTC TCA AAG ATC AAA GAA GGT GAC TAC AAC [CCC]

FIG.2B

340 STOP TRANSFER SEQUENCE 350
LEU PHE ILE PRO VAL ALA VAL MET VAL THR ALA PHE SER GLY LEU ALA PHE LEU ILE TRP
CTC TTC ATT CCT GTA GCC GTC ATG GTC ACC GCA TTC TCG GGG CTG GCA TTT CTC ATT TCG

360 370 372
LEU ALA ARG ARG LEU LYS LYS GLY LYS LYS SER GLN GLU ARG MET ASP ASP PRO TYR OP
CTG GCA AGG CGG TTA AAA AAA GGC AAG AAA TCT CAA GAA AGG ATG GAT GAT CCA TAC TGA

TTTCATCCTTTGTGAAGAAAGCCATGAAGTGCTAAAGACAAACATTGGAATAACGTCAAGTCTCCCGTGAAGA
TTTTACACGACGAGCATCTCCACATTAGAGATGCAGTGTGCTCAACGAATCTGGAAGATTCTTCATGACCAACA
GCTCCCTCCTAATTTCCCTCGCTCATTCATCCCATTAACCCATATCCCATATGTGTCTPATACAGAGTATTTTA
TCATCTTTTCTGTGAGGAACAAGCAAAAGTTACTGTAGAAATATAAGACAGCTGCTTTTACTCTTTCCTAACCT
TGTTTCTAGTCAATTACAGACAGAAAGCTAATGCCAAACACAGTGAAATATGATCCATGAGTAATTGAAACTCAG
ACTCCTTGGCAATAGTAGTACCCCTATGTACATCGACAAAAATCTTTCATTTCACACCTCCAAAGAACAGTGCTTAI
TCAAGTTGGGAAAGTCTCTACTTCTCTGTAGACCCACTATCTGTAGTGACAGCCACTGTAGCTGTTCACATTAACT
TCCCCATCTCTTTTCCCTAGAGATAATTCACACACTGCACCCCATGATGCCACCAACATCAAGAGGAAAA
TCTCCTGCATGAGTTTGTAGTTTGTAGTTTCCCTTCTCTTAATTAGATCTGTATGTTCTTGAAGTCAAGTGTCT
GATGATTATTATAGTTAATGATAACACAACCCACTCTCTTGAGCTGATGTTATGAAGACACACAGGTAGAAAAATTC
CTGGGCTCAGGCTGAGTGACACCCCTTTTCTTCCCTAACATCTTCTACTCAGATAACCTAAATTAAAGATTTCAGGACA
GCTGTCCCCCACTCTTACCATGTCTTTTATAACTTCTCTTAACCTTGCCCAACCTGTAGGCTATCTCATTTTCTCGC
TTCACTCTGCAAGTTTATACATGATGAATTTAAATACAAAAA

		SIGNAL SEQUENCE																																																
mHR	M	V	F	P	W	R	C	E	G	T	Y	W	G	S	R	N	I	L	K	L	W	V	W	T	L	L	C	C	D	F	L	I	H	G	T	H	C	W	T	Y	H	Y	S	E	K	P	M	N	W	
hHR	M	I	F	P	W	K	C	Q	S	T	Q	R	D	L	W	N	I	F	K	L	W	G	W	T	M	L	C	C	D	F	L	A	H	H	G	T	Y	C	W	T	Y	H	Y	S	E	K	P	M	N	W

		LECTIN DOMAIN																																																
mHR	E	N	A	R	K	F	C	K	Q	N	Y	T	D	L	V	A	I	Q	N	K	R	E	I	E	Y	L	E	N	T	L	P	K	S	P	Y	Y	Y	W	I	G	I	R	K	I	G	K	M	W	T	W
hHR	Q	R	A	R	R	E	C	R	D	N	Y	T	D	L	V	A	I	Q	N	K	A	E	I	E	Y	L	E	K	T	L	P	F	S	R	S	Y	Y	W	I	G	I	R	K	I	G	G	I	W	T	W

mHR	V	G	T	N	K	T	L	T	K	E	A	E	N	W	G	A	G	E	P	N	N	K	K	S	K	E	D	C	V	E	I	Y	I	K	R	E	R	D	S	G	K	W	N	D	A	C	H	K	I	R
hHR	V	G	T	N	K	S	L	T	E	E	A	E	N	W	G	D	G	E	P	N	N	K	K	N	K	E	D	C	V	E	I	Y	I	K	R	N	K	D	A	G	K	W	N	D	A	C	H	K	L	

		EGF DOMAIN																																																
mHR	K	A	A	L	C	Y	T	A	S	C	Q	P	G	S	C	N	G	R	G	E	C	V	E	T	I	N	N	H	T	C	I	C	D	A	G	Y	Y	G	P	Q	C	Q	Y	V	V	Q	C	E	P	L
hHR	K	A	A	L	C	Y	T	A	S	C	Q	P	W	S	C	S	G	H	G	E	C	V	E	I	I	N	N	H	T	C	N	C	D	V	G	Y	Y	G	P	Q	C	Q	L	V	I	Q	C	E	P	L

FIG.3A

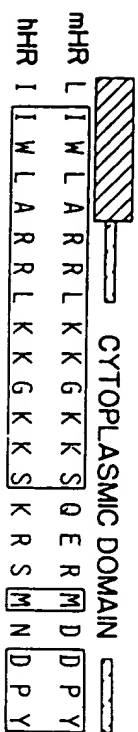
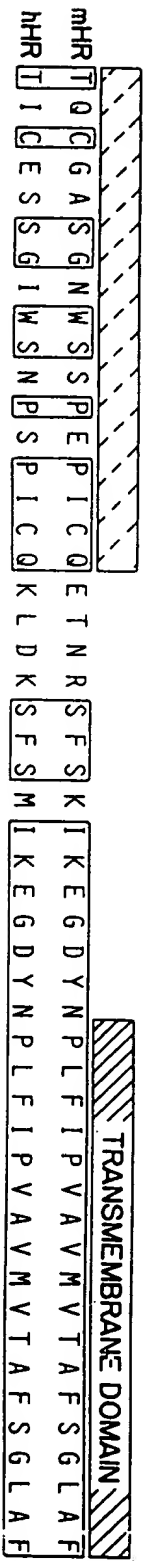
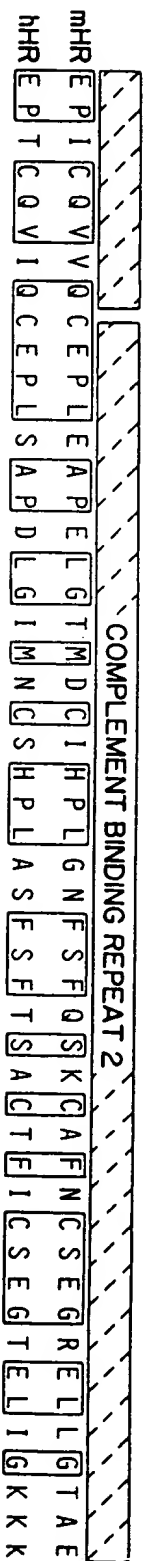
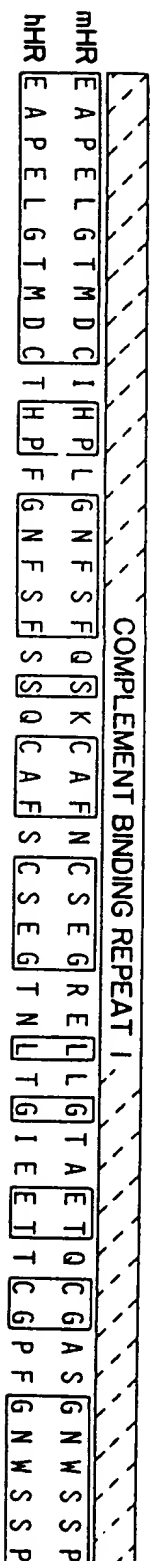


FIG.3B



FIG.4B

FIG.4C

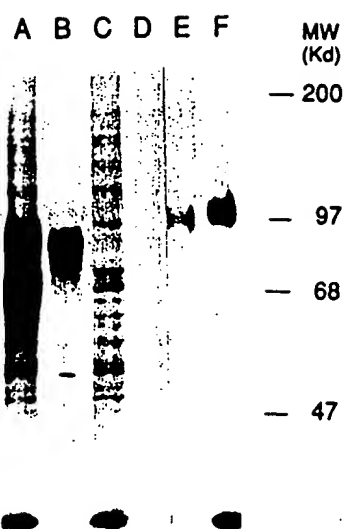


FIG. 5

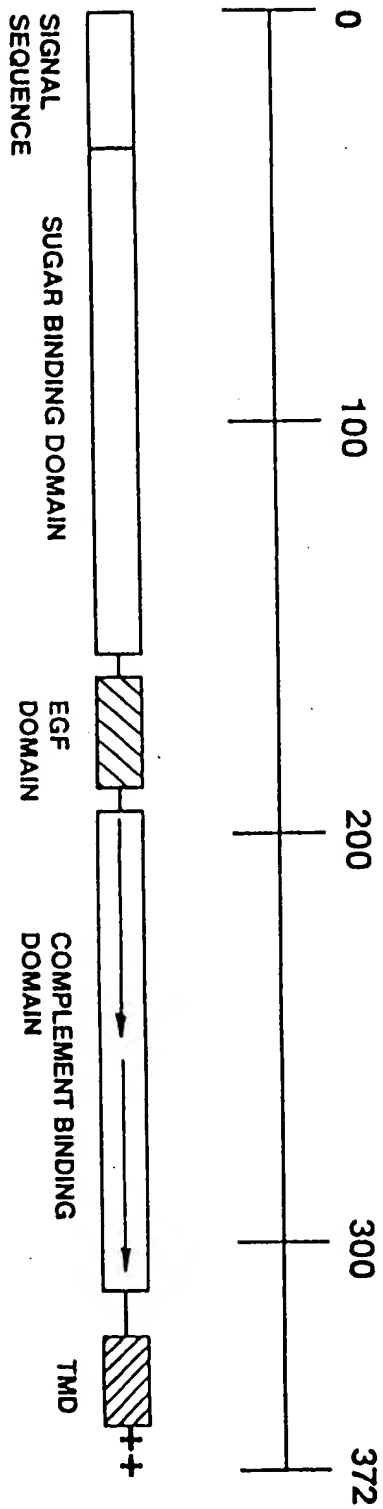


FIG. 6